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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:10:57 ; Search time 185 Seconds
(without alignments)
121.126 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51

Perfect score: 51

Sequence: 1 MLQAGQCQNEVFDLLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring table

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size 8

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	52	9 AEC02032	Amino aci
2	51	100.0	184	3 AAB08843	Amino aci
3	51	100.0	184	3 AAY94001	A human B
4	51	100.0	184	4 AAE09241	Human BCM
5	51	100.0	184	4 AAY71979	Human B c
6	51	100.0	184	4 AAB60698	Human BAF
7	51	100.0	184	4 AAE00506	Human B c
8	51	100.0	184	5 ABB81487	Human BCM
9	51	100.0	184	5 ABP54694	Metastati
10	51	100.0	184	5 AAE28961	Human B-c
11	51	100.0	184	6 AAE35216	Human B-c
12	51	100.0	184	6 ADA49361	Human BCM
13	51	100.0	184	6 ABP60552	Human tum
14	51	100.0	184	6 ABP97717	Amino aci
15	51	100.0	184	7 ADD67527	Human Lyl
16	51	100.0	184	7 ADG43715	Human B-c
17	51	100.0	184	8 ADK00756	Native hu
18	51	100.0	184	8 ADQ94442	Neutrokin
19	51	100.0	184	8 ADP56014	Human BCM
20	51	100.0	184	9 ADW03432	Human PRO
21	51	100.0	184	9 ADZ67760	Human tum
22	51	100.0	184	9 AEA23348	Tumor ant
23	51	100.0	184	9 AEC02031	Amin acid
24	51	100.0	302	4 AAB60699	Mouse IgG

25	51	100.0	302	4 AAE00507	Aae00507 Human BCM
26	51	100.0	302	7 ADG43717	Adg43717 Human B-c
27	48	94.1	51	5 AAE15485	Aae15485 Human B-c
28	48	94.1	181	5 AAE15484	Aae15484 Human B-c
29	48	94.1	184	6 ABR40082	AbR40082 Human Gen
30	48	94.1	283	5 AAE15488	Aae15488 Human BCM
31	48	94.1	288	5 ABG95060	ABg95060 Human tra
32	44	86.3	58	5 AAE15501	Aae15501 Human B c
33	40	78.4	40	9 ADZ67761	Adz67761 Human tum
34	38	74.5	38	9 AEC02033	Aec02033 Amino aci
35	34	66.7	34	5 AAE15486	Aae15486 Human B-c
36	34	66.7	34	6 ADA49366	Ada49366 Human BCM
37	29	56.9	296	9 AEC02042	Aec02042 Amino aci
38	28	54.9	34	9 AEC02025	Aec02025 Formula I
39	28	54.9	34	9 AEC02026	Aec02026 Formula I
40	28	54.9	34	9 AEC02024	Aec02024 Formula I
41	28	54.9	42	6 ABJ38417	Abj38417 TALL-1 re
42	26	51.0	26	7 ADI53060	Adi53060 Human BCM
43	19	37.3	34	9 AEC02020	Aec02020 Formula I
44	19	37.3	34	9 AEC02028	Aec02028 Formula I
45	19	37.3	34	9 AEC02017	Aec02017 Formula I

ALIGNMENTS

RESULT 1

AEC02032

ID AEC02032 standard; peptide; 52 AA.

XX AC AEC02032;

XX AC AEC02032;

XX 20-OCT-2005 (first entry)

XX Amino acid sequence of an extracellular domain of BCMA.

XX APRIL; BAFF; immune disorder; immunomodulator; antinflammatory; cancer;

XX cytostatic; neoplasm; immunosuppressive; therapeutic;

XX B-cell maturation antigen; BCMA.

XX Synthetic.

XX WO2005075511-A1.

XX 18-AUG-2005.

XX 04-AUG-2004; 2004WO-US025247.

XX 29-JAN-2004; 2004US-0540271P.

XX (GETH) GENENTECH INC.

XX Kelley RF, Patel D;

XX WPI; 2005-555932/56.

XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful

XX for treating immune-related disease, cancer or T-cell mediated disease

XX such as graft rejection, graft versus host disease (GVHD) and

XX inflammation.

XX Disclosure; SEQ ID NO 21; 140pp; English.

XX The specification describes polypeptides that bind APRIL or BAFF. The

XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen

XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The

XX polypeptides of the invention are useful for treating immune-related

XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic

XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple

XX sclerosis; or T-cell mediated disease such as graft rejection, graft

XX versus host disease (GVHD) and inflammation. The present sequence

XX represents an extracellular domain of BCMA.

SQ Sequence 52 AA; Query Match 100.0%; Score 51; DB 9; Length 52; Best Local Similarity 100.0%; Pred. No. 1.4e-47; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKG 51
 DB 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKG 51

RESULT 2
 AAB08843
 ID AAB08843 standard; peptide; 184 AA.
 XX AC AAB08843;
 XX DT 02-JAN-2001 (first entry)
 XX DE Amino acid sequence of human.
 XX KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT 57..77
 FT Domain /note= "putative transmembrane domain"
 XX PN WO200050633-A1.
 XX PD 31-AUG-2000.
 XX PF 24-FEB-2000; 2000WO-US004925.
 XX PR 24-FEB-1999; 99US-0121485P.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PI Seed B, Ting A;
 XX WPI; 2000-558405/51.
 XX Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression.
 XX Claim 32; Fig 7A; 53pp; English.
 XX PS
 CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is
 CC a necrosis factor (NF)-kB activator. The method of the invention is used
 CC to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease or septic shock. BCMA is useful for drug
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing
 XX Sequence 184 AA;
 Query Match 100.0%; Score 51; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKG 51
 DB 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKG 51

RESULT 3
 AAY94001
 ID AAY94001 standard; protein; 184 AA.
 XX AC AAY94001;
 XX DT 20-OCT-2000 (first entry)
 XX DE A human BCMA protein, a B cell protein related to TACI.
 XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasms; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX OS Homo sapiens.
 XX PN WO200040716-A2.
 XX PD 13-JUL-2000.
 XX PF 07-JAN-2000; 2000WO-US000396.
 XX PR 07-JAN-1999; 99US-00226533.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Gross JA, Xu W, Madden K, Yee DP;
 XX WPI; 2000-452538/39.
 XX DR N-PSDB; AA58559.
 XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 XX Disclosure; Page 152; 175pp; English.
 XX PS
 CC The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli

Query Match 100.0%; Score 51; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-47; Mismatches 0; Indels 0; Gaps 0;
 Matches 51; Conservative 0

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASVTNSVKG 51
 DB 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASVTNSVKG 51

RESULT 6
 AAB60698
 ID AAB60698 standard; protein; 184 AA.
 XX
 AC AAB60698;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human BAFF receptor (BAFF-R).
 XX
 KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmunity disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; anti-inflammation; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WO-US022507.
 XX
 PR 17-AUG-1999; 99US-0149378P.
 PR 11-FEB-2000; 2000US-0181684P.
 PR 18-FEB-2000; 2000US-0183536P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 PI Thompson J;
 XX
 DR WPI; 2001-202866/20.
 DR N-PSDB; AAF59998.
 XX
 XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lymphoproliferative disorder by administering BAFF-receptor polypeptide,
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 XX
 PS Claim 20; Fig 1; 59pp; English.

The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia,

CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, CC autoimmune disorders and inherited B-cell-associated disorders. The CC present sequence represents human BAFF-R
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 51; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-47; Mismatches 0; Indels 0; Gaps 0;
 Matches 51; Conservative 0

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASVTNSVKG 51
 DB 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASVTNSVKG 51

RESULT 7
 AAE00506
 ID AAE00506 standard; protein; 184 AA.
 XX
 AC AAE00506;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Human B cell maturation protein (BCMA).
 XX
 KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF;
 KW tumour necrosis factor; BCMA; B cell maturation protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200124811-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027579.
 XX
 PR 06-OCT-1999; 99US-0157933P.
 PR 11-FEB-2000; 2000US-0181807P.
 PR 30-JUN-2000; 2000US-0215688P.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
 PI WPI; 2001-266242/27.
 DR N-PSDB; AAD03844.
 XX
 XX Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 PT antagonist.
 XX
 PS Claim 3; Fig 3A; 85pp; English.

The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular

CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is human APRIL-R also referred as BCM or BCM protein
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 51; DB 4; Length 184;

Best Local Similarity 100.0%; Pred. No. 4.1e-47;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCQNEFYDLSLHACIPQLRCSSNTPLTLCQRYCNASVTNSVKG 51

DB 1 MLQMGQCQNEFYDLSLHACIPQLRCSSNTPLTLCQRYCNASVTNSVKG 51

RESULT 8

ID ABB81487 standard; protein; 184 AA.

AC ABB81487;

DT 02-SEP-2002 (first entry)

DE Human BCM receptor related protein SEQ ID NO:7.

XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

XX WO200238766-A2.

XX 16-MAY-2002.

XX 05-NOV-2001; 2001WO-US047018.

XX 07-NOV-2000; 2000US-0246449P.

XX 20-DEC-2000; 2000US-0257131P.

XX 28-JUN-2001; 2001US-0301715P.

XX 29-AUG-2001; 2001US-0315565P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Henne RM, Grant FJ;

XX WPI; 2002-508212/54.

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed

XX Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage

XX renal failure or renal disease and lymphoma.

XX Disclosure; Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for

CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 51; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 4.1e-47;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCQNEFYDLSLHACIPQLRCSSNTPLTLCQRYCNASVTNSVKG 51

DB 1 MLQMGQCQNEFYDLSLHACIPQLRCSSNTPLTLCQRYCNASVTNSVKG 51

RESULT 9

ABP54694

ID. ABP54694 standard; protein; 184 AA.

XX AC ABP54694;

XX 30-DEC-2002 (first entry)

XX Metastatic colorectal cancer-associated polypeptide.

DE Colorectal cancer; metastasis; differential expression; cytostatic;

KW diagnosis; gene therapy; vaccine.

XX Homo sapiens.

XX WO200268677-A2.

XX 06-SEP-2002.

XX 27-FEB-2002; 2002WO-US006001.

XX 27-FEB-2001; 2001US-0272206P.

XX 02-APR-2001; 2001US-0281149P.

XX 17-APR-2001; 2001US-0284555P.

XX (SCSB-) EOS BIOTECHNOLOGY INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Mack DH, Markowitz SD;

XX WPI; 2002-698677/75.

XX N-PSDB; ABQ81560.

XX New genes that are up- or down-regulated in colorectal cancer, useful for

XX diagnosing colorectal cancer in a subject, or for identifying modulators

XX of colorectal cancer-associated proteins and genes for treating

XX colorectal cancer.

XX Claim 8; Page 255; 260pp; English.

XX The present sequence is the protein sequence of a human polypeptide

XX encoded by a gene that exhibits decreased expression in colon cancer-

XX derived metastases compared to normal colon tissue. It is an example of

XX claimed polypeptides that are encoded by genes which are differentially

CC therapeutic value

XX Sequence 184 AA;

SQ

Query Match 100.0%; Score 51; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51
 |||||

Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51
 |||||

RESULT 10

AAE28961

ID AAE28961 standard; protein; 184 AA.

XX

AC AAE28961;

XX

DT 27-JAN-2003 (first entry)

XX

DE Human B-cell maturation antigen (BCMA).

XX

KW Human; tumour; B-cell maturation antigen; transmembrane activator;
 calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
 neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
 non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
 BCMA; multiple myeloma.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1..54

FT /note= "Antigenic epitope"

FT Domain 1..48

FT /note= "Extracellular domain"

FT Region 8..41

FT /note= "Cysteine rich region"

XX

XX WO200266516-A2.

XX

XX 29-AUG-2002.

XX

XX 06-FEB-2002; 2002WO-US003500.

XX

XX 20-FEB-2001; 2001US-0270274P.

XX

XX 12-APR-2001; 2001US-0283447P.

XX

XX (ZYMO) ZYMOGENETICS INC.

XX

XX Kindavogel W;

XX

XX WPI; 2002-723183/78.

XX

XX N-PSDB; AAD46410.

XX

XX B-cell maturation antigen and transmembrane activator and calcium-
 modulator and cyclophilin ligand-interactor, useful for treating
 disorders e.g. inflammation or lymphoma.

XX

XX Disclosure; Page 63; 67pp; English.

XX

XX The invention relates to the manufacture of a composition for inhibiting
 the proliferation of tumour cells. The method involves using an antibody
 component that binds both the B-cell maturation antigen (BCMA) and the
 transmembrane activator and calcium-modulator and cyclophilin ligand-
 interactor (TACI). BCMA and TACI binding antibody compositions are useful
 for inhibiting proliferation of tumour cells, particularly inhibiting
 ZTNF4 activity in a mammal associated with increased endogenous antibody
 production or a disorder consisting of neoplasm, chronic lymphocytic
 leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
 lymphoproliferative disease or light chain gammopathy or inflammation
 e.g. asthma. The invention is also useful in gene therapy. The present is
 human BCMA protein

XX Sequence 184 AA;

SQ

Query Match 100.0%; Score 51; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51
 |||||

Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKG 51
 |||||

RESULT 11

AAE35216

ID AAE35216 standard; protein; 184 AA.

XX

AC AAE35216;

XX

DT 28-MAY-2003 (first entry)

XX

DE Human B-cell maturation receptor (BCMA) protein.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 B-cell maturation receptor; BCMA; receptor.

XX

OS Homo sapiens.

XX

XX WO200294852-A2.

XX

XX 28-NOV-2002.

XX

XX 20-MAY-2002; 2002WO-US015910.

XX

XX 24-MAY-2001; 2001US-0293343P.

XX

XX (ZYMO) ZYMOGENETICS INC.

XX

XX Rixon MW, Gross JA;

XX

XX WPI; 2003-148455/14.

XX

XX N-PSDB; AAD53754.

XX

XX Transmembrane activator and calcium modulator and cyclophilin ligand-
 interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
 diabetes, comprises a TACI receptor group and an immunoglobulin group.

XX

XX Disclosure; Col 100; 71pp; English.

XX

XX The invention relates to fusion proteins comprising transmembrane
 activator and calcium modulator and cyclophilin ligand-interactor (TACI)
 receptor group that binds tumour necrosis factor-like protein (ZTNF2) or
 ZTNF4; and an immunoglobulin group comprising a constant region of an
 immunoglobulin. The invention is used to manufacture a medicament for
 inhibiting the proliferation of tumour cells in a mammalian subject. The
 composition comprising the fusion protein may also be used in treating
 autoimmune diseases (e.g. systemic lupus erythematosus, multiple
 sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
 diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
 rejection, anaemia and septic shock. The fusion proteins are also used in
 gene therapy. The present sequence is human B-cell maturation receptor
 (BCMA) protein used in the invention

XX

XX Sequence 184 AA;

SQ

Query Match 100.0%; Score 51; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4.1e-47;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
 |||||
 DB 1 MLQAGQCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
 |||||

RESULT 12

ADA49361
 ID ADA49361 standard; protein; 184 AA.

AC ADA49361;

XX 20-NOV-2003 (first entry)

XX Human BCMA protein.

XX human; TALL-1; antagonist; immunosuppressive; antirheumatic;
 KW antiinflammatory; antiarthritic; dermatological; antidiabetic;
 KW neuroprotective; antithyroid; antipruritic; nephrotropic; vasotropic;
 KW vaccine; autoimmune disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; insulin dependent diabetes mellitus;
 KW multiple sclerosis; myasthenia gravis; Grave's disease;
 KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
 KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.

XX Homo sapiens.

XX WO2003035846-A2.

XX 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034376.

XX 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348962P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Zhang G, Shu H, Liu Y, Xu L;

XX WPI; 2003-403345/38.

XX N-PSDB; ADA49360.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological

PT activity in mammal, has a modification in the region connecting beta

PT strands D and E that reduces the biological activity of TALL-1

PT antagonist.

XX Claim 62; Page 613; 618pp; English.

XX The invention relates to a novel TALL-1 antagonist protein, comprising a
 CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting tbrgr; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, antirheumatic, antiinflammatory, antithyroid, antipruritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipruritic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents human BCMA.

XX Sequence 184 AA;

Query Match 100.0%; Score 51; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 4.1e-47;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
 |||||

DB 1 MLQAGQCSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
 |||||

RESULT 13

ABP60552

ID ABP60552 standard; protein; 184 AA.

XX AC ABP60552;

XX 28-MAR-2003 (first entry)

XX Human tumour necrosis factor BCMA.

XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;
 KW antiarthritic; cycostatic; antianaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; antiallergic; tuberculostatic; antidiabetic;
 KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thymomimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; BCMA; tumour necrosis factor.

XX Homo sapiens.

XX WO200294192-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-US016106.

XX 24-MAY-2001; 2001US-0293100P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM;

XX WPI; 2003-156740/15.

XX Novel isolated antibody that immunospecifically binds tumor necrosis
 PT factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.

XX Disclosure; Page 222; 225pp; English.

XX The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC antiinflammatory, antirheumatic, antithyroid, cycostatic, antianaemic,
 CC antiallergic, antidiabetic, neuroprotective, ophthalmological,
 CC tuberculostatic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thymomimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents


```

CC the tumour necrosis factor BCMA
XX
SQ Sequence 184 AA;

  Query Match      100.0%; Score 51; DB 6; Length 184;
  Best Local Similarity 100.0%; Pred. No. 4.1e-47;
  Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCRLCSSNTPPLTCORYCNASVTSVKG 51
   |||||
Db 1 MLQAGQCSQNEYFDSLHACIPQCRLCSSNTPPLTCORYCNASVTSVKG 51

RESULT 14
ABP97717
ID ABP97717 standard; protein; 184 AA.
XX
AC ABP97717;
XX
DT 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of human BCMA receptor.
XX
KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus; BCMA.
XX
OS Homo sapiens.
XX
PN WO2003014294-A2.
XX
PD 20-FEB-2003.
XX
PF 24-JUL-2002; 2002WO-US023487.
XX
PR 03-AUG-2001; 2001US-0310114P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Dixit V, Grewal I, Ridgway J, Yan M;
XX
WPI; 2003-256560/25.
DR N-PSDB; ABZ68871.
XX
New nucleic acid encoding a TACIS or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus.
XX
PS Disclosure; Fig 2; 153pp; English.
XX
The present sequence represents a human BCMA polypeptide. The
CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
CC preparing a composition for treating systemic lupus erythematosus
XX
SQ Sequence 184 AA;

  Query Match      100.0%; Score 51; DB 6; Length 184;
  Best Local Similarity 100.0%; Pred. No. 4.1e-47;
  Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCRLCSSNTPPLTCORYCNASVTSVKG 51
   |||||
Db 1 MLQAGQCSQNEYFDSLHACIPQCRLCSSNTPPLTCORYCNASVTSVKG 51

RESULT 15
ADD67527
ID ADD67527 standard; protein; 184 AA.
XX
AC ADD67527;
XX

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```

DT 15-JAN-2004 (first entry)
XX
DE Human Iy1732P protein SEQ ID NO:4.
XX
KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
KW vaccine; immunotherapy; cancer; multiple myeloma cell;
KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003062401-A2.
XX
PD 31-JUL-2003.
XX
PF 22-JAN-2003; 2003WO-US002353.
XX
PR 22-JAN-2002; 2002US-00057475.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
PI Carter L, McNeill PD;
XX
WPI; 2003-598749/56.
DR N-PSDB; ADD67526.
XX
New hematological malignancy-related genes and polypeptides, useful for
PT screening anti-cancer agents, and generating antibodies or
PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
PT lymphocytic leukemia.
XX
Claim 9; SEQ ID NO 4; 307pp; English.
XX
The present invention describes an isolated polynucleotide (1), which is
CC overexpressed in haematological malignancies, and which encodes a
CC polypeptide or an immunogenic fragment of the polypeptide. Also
CC described: (1) an isolated polypeptide; (2) an expression vector
CC comprising (1) operably linked to an expression control sequence; (3) a
CC host cell comprising an expression vector; (4) an isolated antibody that
CC specifically binds to the polypeptide or its immunogenic fragment; and
CC (5) immunoconjugates comprising the antibody above, or an antibody that
CC specifically binds to a polypeptide, or its immunogenic fragment, encoded
CC by (1). (1) has cytostatic and immunostimulant activities, and can be
CC used in vaccines and immunotherapy. The immunoconjugates are useful in a
CC the manufacture of a medicament, particularly as active ingredients in a
CC composition for treating cancer, e.g. multiple myeloma cell, chronic
CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
CC primates, goats, bovines, equines, porcines, lupines, canines or felines.
CC The polynucleotide (1) or polypeptide can be used for screening anti-
CC cancer agents, and generating antibodies or immunoconjugates for treating
CC or preventing the above-mentioned diseases. The polynucleotide,
CC polypeptide or antibody can be used for detecting, diagnosing or
CC prognosticating the haematological malignancies described above. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 184 AA;

  Query Match      100.0%; Score 51; DB 7; Length 184;
  Best Local Similarity 100.0%; Pred. No. 4.1e-47;
  Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCRLCSSNTPPLTCORYCNASVTSVKG 51
   |||||
Db 1 MLQAGQCSQNEYFDSLHACIPQCRLCSSNTPPLTCORYCNASVTSVKG 51

Search completed: March 2, 2006, 04:23:29
Job time : 187 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: March 2, 2006, 04:23:47 ; Search time 38 Seconds
(without alignments)
129.133 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51
Perfect score: 51
Sequence: 1 MLQAGCQSQNEYFDSLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring-table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.*
1: Piri:.*
2: Piri2:.*
3: Piri3:.*
4: Piri4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	184	2 S43486	B-cell maturation
2	7	13.7	309	2 E72365	conserved hypothet
3	7	13.7	5188	2 B85547	probable RTX famil
4	7	13.7	5291	2 F90696	hypothetical prote
5	6	11.8	113	2 E72242	hypothetical prote
6	6	11.8	129	2 A81187	type IV pilin prot
7	6	11.8	148	2 B58345	myoglobin - tremet
8	6	11.8	223	2 S16652	hypothetical prote
9	6	11.8	237	2 T24407	hypothetical prote
10	6	11.8	240	2 A96697	protein FLN21.18
11	6	11.8	245	2 T36127	probable ribonucle
12	6	11.8	249	2 T45217	rec7 protein - fis
13	6	11.8	257	2 E89124	protein K07C11.1
14	6	11.8	269	2 AC0404	probable deor-fam
15	6	11.8	283	2 C86535	hypothetical prote
16	6	11.8	283	2 T172087	hypothetical prote
17	6	11.8	303	2 T17774	hypothetical prote
18	6	11.8	311	2 C69464	carboxylesterase
19	6	11.8	321	1 Q0EC15	hypothetical 34K p
20	6	11.8	321	2 F91104	hypothetical prote
21	6	11.8	321	2 A85950	hypothetical prote
22	6	11.8	327	2 S61660	probable membrane
23	6	11.8	338	2 A82209	conserved hypothet
24	6	11.8	339	2 T41126	meiotic recombina
25	6	11.8	340	2 B96632	hypothetical prote
26	6	11.8	353	2 H75446	(S)-2-hydroxy-acid
27	6	11.8	398	1 OKBYC3	protein kinase (EC
28	6	11.8	404	2 S64944	hypothetical prote
29	6	11.8	460	2 H69095	carbon monoxide de

30	6	11.8	479	2 T30794	hypothetical prote
31	6	11.8	479	2 T28480	hypothetical prote
32	6	11.8	479	2 H72155	CiL protein - vari
33	6	11.8	479	2 E42508	EiL protein - vacc
34	6	11.8	479	2 D36841	EiL protein - vari
35	6	11.8	488	2 S68892	lysine-tRNA ligase
36	6	11.8	499	2 A28997	triacylglycerol li
37	6	11.8	539	2 T01513	CTP synthase (EC 6
38	6	11.8	553	2 S53080	hypothetical prote
39	6	11.8	554	2 C69161	sensory transducti
40	6	11.8	639	2 S62567	hypothetical prote
41	6	11.8	643	2 D96775	hypothetical prote
42	6	11.8	659	2 T11641	hypothetical prote
43	6	11.8	677	2 S16003	rpIC protein - xan
44	6	11.8	680	2 T29204	hypothetical prote
45	6	11.8	752	2 G95094	hypothetical prote

ALIGNMENTS

RESULT 1

S43486
B-cell maturation factor - human
N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43486; S31208; S36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidir
A;Reference number: S43486; MUID:94218235; PMID:8165126
A;Accession: S43486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <LA3>
A;Cross-references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z29574; NID:9471244; PI
R;Laabi, Y.; Gras, M.P.; Carbone, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,
EMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PI
A;Accession: S36661
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 4-184 <LA3>
A;Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955
C;Genetics:
A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 51; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGCQSQNEYFDSLHAICQLRCSNTPTPLTCQRYCNASVTNSVKG 51
Db 1 MLQAGCQSQNEYFDSLHAICQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 2

E72365
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: E72365
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: E72365
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-309 <ARN>
 A:Cross-references: UNIPROT:Q9WY9; UNIPARC:UPI00000C13FC; GB:AE001728; GB:AE000512; NID:10360571
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM0519

Query Match 13.7%; Score 7; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSLL 18
 Db 165 EYFDSLL 171

RESULT 3
 B85547
 probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain C)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 A:Accession: B85547
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Bowers, J.; Rhee, S.; White, O.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: B85547
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5188 <STO>
 A:Cross-references: UNIPROT:Q8X4H5; UNIPARC:UPI000011021E; GB:AE005174; NID:gl2513368; F00696
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 20615

Query Match 13.7%; Score 7; DB 2; Length 5188;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ASVTNSV 49
 Db 1814 ASVTNSV 1820

RESULT 4
 F00696
 hypothetical protein ECe0542 [imported] - Escherichia coli (strain O157:H7, substrain R)
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 A:Accession: F00696
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: F00696
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5291 <HAY>
 A:Cross-references: UNIPROT:Q8X2T1; UNIPARC:UPI000011021F; GB:BA000007; PIDN:BA033965.1; F00696
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECe0542

Query Match 13.7%; Score 7; DB 2; Length 5291;

Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ASVTNSV 49
 Db 1814 ASVTNSV 1820

RESULT 5
 B72242
 hypothetical protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 A:Accession: B72242
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, J.; Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: B72242
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-113 <ARN>
 A:Cross-references: UNIPROT:Q9X1M0; UNIPARC:UPI00000C126C; GB:AE001800; GB:AE000512; NID:10360571
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1534
 C:Superfamily: Thermotoga maritima hypothetical protein TM1534

Query Match 11.8%; Score 6; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 VTNSVK 50
 Db 55 VTNSVK 60

RESULT 6
 A81187
 type IV pilin protein NMB0547 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 A:Accession: A81187
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vamathevan, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: A81187
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-129 <TET>
 A:Cross-references: UNIPROT:Q9XON9; UNIPARC:UPI00000C44EE; GB:AE002410; GB:AE002098; NID:10710307
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0547

Query Match 11.8%; Score 6; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QNEYFD 15
 Db 74 QNEYFD 79

RESULT 7
 B58345
 myoglobin - tremetode (Isoparorchis hypselobagri)

C:Species: Isoparorchis hypselobagri
 C>Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 12-Jul-2004
 C:Accession: B58345
 R:Rashid, A.R.; Van Hauwaert, M.; Haque, M.; Siddiqi, A.H.; Lasters, I.; De Mayer, M.; C
 submitted to the Protein Sequence Database, October 1996
 A:Description: Trematode myoglobins: functional molecules with a distal tyrosine.
 A:Reference number: A58345
 A:Accession: B58345
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-148 <RAS>
 A:Cross-references: UNIPROT:P80722; UNIPARC:UPI0000012B54D
 A>Note: monomeric myoglobin with a tyrosine at position B10 and E7(distal position) res
 C:Superfamily: trematode myoglobin; globin homology

Query Match 11.8%; Score 6; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FDSLTH 19
 |||||
 Db 7 FDSLTH 12

RESULT 8

S16652
 hypothetical protein_223 - Escherichia coli retron Ec86
 C:Species: Escherichia coli retron Ec86
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Jul-1998
 C:Accession: S16652
 R:Lim, D.

Mol. Microbiol. 5, 1863-1872, 1991
 A:Title: Structure of two retrons of Escherichia coli and their common chromosomal inser
 A:Reference number: S16652; MUID:92114764; PMID:1722556
 A:Accession: S16652
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-223 <LIM>
 A:Cross-references: UNIPARC:UPI000017CAC0; EMBL:X60206
 A:Experimental source: strain B

Query Match 11.8%; Score 6; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRCSSN 31
 |||||
 Db 152 LRCSSN 157

RESULT 9

T24407
 hypothetical protein T03F7.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T24407
 R:Mortimore, B.
 submitted to the EMBL Data Library, June 1996

A:Reference number: Z19887
 A:Accession: T24407
 A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-237 <WIL>
 A:Cross-references: UNIPROT:Q22118; UNIPARC:UPI00000827F9; EMBL:Z74041; PIDN:CAA98521.1;
 A:Experimental source: clone T03F7
 C:Genetics:
 A:Gene: CESP:T03F7.6
 A:Map position: 5
 A:Introns: 12/1; 53/1; 117/3; 168/3; 191/3

Query Match 11.8%; Score 6; DB 2; Length 237;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SQNEYF 14
 |||||
 Db 224 SQNEYF 229

RESULT 10

A96697
 protein FLN21.18 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: A96697
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.
 ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A96697
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-240 <STO>
 A:Cross-references: UNIPROT:Q9FYF7; UNIPARC:UPI00000013F1; GB:AE005173; NID:99828625; P
 C:Genetics:
 A:Gene: FLN21.18
 A:Map position: 1

Query Match 11.8%; Score 6; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 VTNSVK 50
 |||||
 Db 142 VTNSVK 147

RESULT 11

T36127
 probable ribonuclease PH - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T36127
 R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, July 1999

A:Reference number: Z21598
 A:Accession: T36127
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-245 <SEE>
 A:Cross-references: UNIPROT:Q9S2H7; UNIPARC:UPI0000134469; EMBL:AL096852; PIDN:CAB50985
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: rph; SCORDB:SCEI9A.04c
 C:Superfamily: tRNA nucleotidyltransferase

Query Match 11.8%; Score 6; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CNASVT 46
 |||||
 Db 40 CNASVT 45

RESULT 12

T45217
 rec7 protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
R;lin, Y.
Genetics 132, 75-85, 1992
A;Title: Meiotically induced rec7 and rec8 schizosaccharomyces pombe genes.
A;Reference number: Z22941; MUID:93012935; PMID:1339382
A;Accession: T45217
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-249 <LIN>
A;Cross-references: UNIPARC:UPI000017B220; EMBL:M85297; NID:g173451; PIDN:AAA53333.1; PIDN:AAA53333.1; PIDN:AAA53333.1; PIDN:AAA53333.1
C;Genetics:
A;Gene: rec7
C;Function:
A;Description: required for meiotic intragenic recombination but not for mitotic recombination

Query Match 11.8%; Score 6; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 SNTTPLL 35
|||||
DB 110 SNTTPLL 115

RESULT 13
E89124
protein K07C11.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89124
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes.
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999.
A;Accession: E89124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Cross-references: UNIPROT:Q21272; UNIPARC:UPI0000077A84; GB:chr_V; PIDN:AAA96181.1; PIDN:AAA96181.1; PIDN:AAA96181.1; PIDN:AAA96181.1
C;Genetics:
A;Gene: K07C11.1
A;Map position: 5
C;Superfamily: paired box transcription factor Pax-8; paired box homology

Query Match 11.8%; Score 6; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 SSNTTTP 34
|||||
DB 242 SSNTTTP 247

RESULT 14
AC0404
probable deor-family regulatory protein YPO3327 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0404
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, N.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0404
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-269 <KUR>
A;Cross-references: UNIPROT:Q82B56; UNIPARC:UPI000000DC895; GB:AL590842.PIDN:CAC92559.1; PIDN:CAC92559.1; PIDN:CAC92559.1; PIDN:CAC92559.1

GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:38:58 ; Search time 164 Seconds
(without alignments)
129.935 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51

Perfect score: 51

Sequence: 1 MLQMAQCQSQNEYFDSLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring table:  Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pcp:
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	51	100.0	184	4	US-10-077-438-1
2	51	100.0	184	4	US-10-077-438-7
3	51	100.0	184	4	US-10-077-137-1
4	51	100.0	184	4	US-10-077-137-7
5	51	100.0	184	4	US-10-068-725-2
6	51	100.0	184	4	US-10-151-882-47
7	51	100.0	184	4	US-10-115-192-8
8	51	100.0	184	4	US-10-008-063-7
9	51	100.0	184	4	US-10-152-363A-27
10	51	100.0	184	4	US-10-216-074-11
11	51	100.0	184	4	US-10-087-080-39
12	51	100.0	184	4	US-10-742-634-9
13	51	100.0	184	5	US-10-626-914-6
14	51	100.0	184	5	US-10-485-489-6
15	51	100.0	184	5	US-10-861-049-27
16	51	100.0	184	5	US-10-989-826-46
17	51	100.0	184	6	US-11-021-874-27
18	51	100.0	302	4	US-10-115-192-12
19	48	94.1	51	3	US-09-854-864-6
20	48	94.1	51	3	US-09-855-158-6
21	48	94.1	181	3	US-09-854-864-5
22	48	94.1	181	3	US-09-855-158-5
23	48	94.1	283	3	US-09-854-864-9
24	48	94.1	283	3	US-09-855-158-9
25	44	86.3	58	3	US-09-854-864-21
26	44	86.3	58	3	US-09-855-158-21
27	37	72.5	207	4	US-10-077-438-3

28	37	72.5	207	4	US-10-077-137-3	Sequence 3, Appli
29	34	66.7	34	3	US-09-854-864-7	Sequence 7, Appli
30	34	66.7	34	3	US-09-855-158-7	Sequence 7, Appli
31	34	66.7	81	3	US-09-854-864-13	Sequence 13, Appli
32	34	66.7	81	3	US-09-855-158-13	Sequence 13, Appli
33	28	54.9	42	4	US-10-145-206-197	Sequence 197, App
34	10	19.6	117	3	US-09-854-864-12	Sequence 12, Appli
35	10	19.6	117	3	US-09-855-158-12	Sequence 12, Appli
36	10	19.6	185	3	US-09-854-864-11	Sequence 11, Appli
37	10	19.6	185	3	US-09-855-158-11	Sequence 11, Appli
38	10	19.6	185	4	US-10-216-074-17	Sequence 17, Appli
39	10	19.6	281	3	US-09-854-864-10	Sequence 10, Appli
40	10	19.6	281	3	US-09-855-158-10	Sequence 263362,
41	7	13.7	76	4	US-10-425-115-263362	Sequence 221552,
42	7	13.7	84	4	US-10-424-599-221552	Sequence 342318,
43	7	13.7	255	4	US-10-425-115-342318	Sequence 73128, A
44	7	13.7	267	4	US-10-425-114-73128	Sequence 30700, A
45	7	13.7	712	5	US-10-450-763-30700	

ALIGNMENTS

RESULT 1
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 184
; ORGANISM: homo sapien
US-10-077-438-1
Query Match 100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQMAQCQSQNEYFDSLHAICPQLRCSNTPLTCQRYCNASVTNSVKG 51
DB 1 MLQMAQCQSQNEYFDSLHAICPQLRCSNTPLTCQRYCNASVTNSVKG 51
RESULT 2
US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg

```
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
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Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
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RESULT 3
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
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RESULT 4
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
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RESULT 6

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Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
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RESULT 5
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
Db 1 MLQAGQCSQNEYFDSLHACIPCOLRCSNTTPTTCORYCNASVTNSVKG 51
|||||
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US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF594
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 7
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match      100.0%; Score 51; DB 4; Length 184;
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Gross, Jane A.
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
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US-10-008-063-7
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 9
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51

RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
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Db 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51

RESULT 11
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1el Methods of Diagnosis of Metastatic Colorectal Cancer
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
US-10-087-080-39

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51
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Db 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51

RESULT 12
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Thereof
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51

RESULT 13
US-10-626-914-6
; Sequence 6, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHAKAPAI, ANAN
; APPLICANT: GREWAL, IQBAL
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-6

Query Match      100.0%; Score 51; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51
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Db 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51

RESULT 14
US-10-485-489-6
; Sequence 6, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: TACIs and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-6

Query Match      100.0%; Score 51; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MLQWAGQCSQNEFYDLSLLHACIPQLRCSSNTPLTLCQRYCNASVTNSVKG 51

RESULT 15

US-10-861-049-27
 ; Sequence 27, Application US/10861049
 ; Publication No. US20050095243A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrew Chan
 ; APPLICANT: Qian Gong
 ; APPLICANT: Flavius Martin
 ; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
 ; FILE REFERENCE: P2040RIUS
 ; CURRENT APPLICATION NUMBER: US/10/861,049
 ; CURRENT FILING DATE: 2004-06-04
 ; PRIOR APPLICATION NUMBER: US 60/476,531
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: US 60/476,481
 ; PRIOR FILING DATE: 2003-06-05
 ; PRIOR APPLICATION NUMBER: US 60/476,414
 ; PRIOR FILING DATE: 2003-06-05
 ; NUMBER OF SEQ ID NOS: 145
 ; SEQ ID NO 27
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-861-049-27

Query Match 100.0%; Score 51; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.1e-45;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEFYDLSLLHACIPQLRCSSNTPLTLCQRYCNASVTNSVKG 51
 Db 1 MLQWAGQCSQNEFYDLSLLHACIPQLRCSSNTPLTLCQRYCNASVTNSVKG 51

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 Job time : 165 secs

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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:39:33 ; Search time 21 Seconds
(without alignments)
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Perfect score: 51
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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	51	100.0	184	US-10-742-634-9
2	51	100.0	184	US-10-967-527A-8
3	51	100.0	184	US-11-242-294-27
4	40	78.4	40	US-10-967-527A-9
5	10	19.6	185	US-10-967-527A-10
6	7	13.7	5291	US-11-052-554A-281
7	6	11.8	221	US-11-100-183-37
8	6	11.8	313	US-11-098-686-10357
9	6	11.8	379	US-11-072-512-3298
10	6	11.8	398	US-11-132-142-7
11	6	11.8	572	US-11-072-512-3907
12	6	11.8	605	US-10-689-742-140
13	6	11.8	668	US-11-087-099-5101
14	6	11.8	766	US-10-821-234-1691
15	6	11.8	800	US-11-072-512-3534
16	6	11.8	1137	US-11-012-762-70
17	6	11.8	1461	US-11-052-554A-283
18	6	11.8	5405	US-11-108-172-1116
19	5	9.8	8	US-11-045-024-496
20	5	9.8	8	US-11-045-024-1697
21	5	9.8	8	US-11-045-024-1698
22	5	9.8	8	US-11-045-024-3636
23	5	9.8	8	US-11-045-024-4379
24	5	9.8	8	US-11-045-024-4380
25	5	9.8	8	US-11-045-024-6787

26	5	9.8	8	7	US-11-045-024-6953	Sequence 6953, Ap
27	5	9.8	8	7	US-11-045-024-7898	Sequence 7898, Ap
28	5	9.8	8	7	US-11-045-024-12102	Sequence 12102, A
29	5	9.8	8	7	US-11-045-024-12785	Sequence 12785, A
30	5	9.8	8	7	US-11-045-024-265	Sequence 265, App
31	5	9.8	8	7	US-11-045-024-643	Sequence 643, App
32	5	9.8	8	7	US-11-045-024-644	Sequence 644, App
33	5	9.8	8	7	US-11-045-024-3241	Sequence 3241, App
34	5	9.8	8	7	US-11-045-024-4503	Sequence 4503, Ap
35	5	9.8	8	7	US-11-045-024-6790	Sequence 6790, Ap
36	5	9.8	8	7	US-11-045-024-6958	Sequence 6958, Ap
37	5	9.8	8	7	US-11-045-024-10213	Sequence 10213, A
38	5	9.8	8	7	US-11-045-024-12084	Sequence 12084, A
39	5	9.8	8	7	US-11-045-024-13797	Sequence 13797, A
40	5	9.8	8	7	US-11-045-024-13801	Sequence 13801, A
41	5	9.8	8	7	US-11-045-024-13803	Sequence 13803, A
42	5	9.8	8	7	US-11-136-079-713	Sequence 713, App
43	5	9.8	8	7	US-11-136-079-736	Sequence 736, App
44	5	9.8	10	7	US-11-152-747-30	Sequence 30, Appl
45	5	9.8	10	7	US-11-045-024-303	Sequence 303, App

ALIGNMENTS

RESULT 1
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20050249671A9

; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokinine-alpha Conjugate, Neutrokinine-alpha Complex, and Uses T
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match 100.0%; Score 51; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.3e-48;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCSQNEFYDLSLLHACIPQLCRCSNTPLTCQRYCNASVTNSVKG 51
DB 1 MLQMGQCSQNEFYDLSLLHACIPQLCRCSNTPLTCQRYCNASVTNSVKG 51

RESULT 2
US-10-967-527A-8
; Sequence 8, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18

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; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 184
; TYPE: prt
; ORGANISM: homo sapiens
; US-10-967-527A-8

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Query Match 100.0%; Score 51; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. NO. 8.3e-48;
Matches 51; Conservative 0; Mismatches 0; Indels

Qy .
1 MLQWAGQCSQNEYFDSLHLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
Dd .
1 MLQWAGQCSQNEYFDSLHLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51

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RESULT 3
US-11-242-294-27
; Sequence 27, Application US/11242294
; Publication No. US20060034852A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/11/242,294
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/10/152,363
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-294-27

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Query Match      100.0%; Score 51; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.3e-48;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MLQWAGQCSQNEYFDLSLTHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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Db 1 MLQWAGQCSQNEYFDLSLTHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51

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RESULT 4
US-10-967-527A-9
; Sequence 9, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Znf14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 40
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:

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; NAME/KEY: DOMAIN
; LOCATION: (1)...(40)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-9

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Query Match      78.4%; Score 40; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.5e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  GGCSONEYFDSLHACIPCOLRGSSNTPPLTCORYCNASV 40
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RESULT 5
US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication NO. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 185
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-10

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Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EYFDSLHAC 21
Db 9 EYFDSLHAC 18

RESULT 6
US-11-052-554A-281
; Sequence 281, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 281
; LENGTH: 5291
; TYPE: prt
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-281

Query Match 13.7%; Score 7; DB 7; Length 5291;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels

; FEATURE:

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QY 43 ASVTSV 49
Db 1814 ASVTSV 1820

RESULT 7
US-11-100-183-37
; Sequence 37, Application US/11100183
; Publication No. US20050272074A1
; GENERAL INFORMATION:
; APPLICANT: Strategene California
; TITLE OF INVENTION: Compositions And Methods For Reverse Transcription
; FILE REFERENCE: 25436/2452
; CURRENT APPLICATION NUMBER: US/11/100,183
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/559,810
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-11-100-183-37

Query Match 11.8%; Score 6; DB 7; Length 231;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 DSLHA 20
Db 118 DSLHA 123

RESULT 8
US-11-098-686-10357
; Sequence 10357, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10357
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10357

Query Match 11.8%; Score 6; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ASVTSV 48
Db 135 ASVTSV 140

RESULT 9
US-11-072-512-3298
; Sequence 3298, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
```

```
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKI, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3298
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3298

Query Match 11.8%; Score 6; DB 7; Length 379;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSL 17
Db 163 EYFDSL 168

RESULT 10
US-11-132-142-7
; Sequence 7, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Saccharomyces sp.
US-11-132-142-7

Query Match 11.8%; Score 6; DB 7; Length 398;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CSSNTP 33
Db 42 CSSNTP 47
```

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RESULT 11
US-11-072-512-3907
; Sequence 3907, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3907
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3907

Query Match      11.8%; Score 6; DB 7; Length 572;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EYFDSL 17
Db      163 EYFDSL 168

RESULT 12
US-10-689-742-140
; Sequence 140, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-689-742-140

Query Match      11.8%; Score 6; DB 7; Length 572;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EYFDSL 17
Db      163 EYFDSL 168

RESULT 13
US-11-087-099-5101
; Sequence 5101, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5101
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Petunia x hybrida
US-11-087-099-5101

Query Match      11.8%; Score 6; DB 7; Length 668;
Best Local Similarity 100.0%; Pred.No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 SSNTPP 34
Db      216 SSNTPP 221

RESULT 14
US-10-821-234-1691
; Sequence 1691, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Targ, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1691
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1691

Query Match      11.8%; Score 6; DB 6; Length 766;
Best Local Similarity 100.0%; Pred.No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LQMAQ 7
Db      31 LQMAQ 36

RESULT 15
US-11-072-512-3534
; Sequence 3534, Application US/11072512
; Publication No. US20060029945A1
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; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAWATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3534
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3534

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Query Match      11.8%; Score 6; DB 7; Length 800;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      7 QCSQNE 12
Db      353 QCSQNE 358

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Search completed: March 2, 2006, 04:42:39
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:27:47 ; Search time 46 Seconds
(without alignments)
91.662 Million cell updates/sec

Title: US-10-077-438-1_COPY_1_51

Perfect score: 51

Sequence: 1 MLQWGCQSQNEVFDLLHA.....TPPLTCQRYCNASVTNSVKG 51

Scoring table: 

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/PCTRUS COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	184	2	US-09-565-423-11
2	51	100.0	192	2	US-09-949-016-11115
3	48	94.1	51	2	US-09-854-864-6
4	48	94.1	181	2	US-09-854-864-5
5	48	94.1	283	2	US-09-854-864-9
6	44	86.3	58	2	US-09-854-864-21
7	34	66.7	34	2	US-09-854-864-7
8	34	66.7	81	2	US-09-854-864-13
9	10	19.6	117	2	US-09-854-864-12
10	10	19.6	185	2	US-09-565-423-17
11	10	19.6	185	2	US-09-854-864-11
12	10	19.6	281	2	US-09-854-864-10
13	6	11.8	29	2	US-09-270-767-60339
14	6	11.8	62	2	US-09-621-976-5704
15	6	11.8	74	2	US-09-510-252-2
16	6	11.8	80	2	US-09-248-796A-26829
17	6	11.8	110	2	US-09-248-796A-26879
18	6	11.8	111	2	US-09-270-767-44871
19	6	11.8	165	2	US-09-270-767-35026
20	6	11.8	165	2	US-09-270-767-50243
21	6	11.8	172	2	US-09-252-991A-28241
22	6	11.8	179	2	US-09-252-991A-25925
23	6	11.8	197	2	US-09-252-991A-23579
24	6	11.8	201	2	US-09-248-796A-19314
25	6	11.8	233	2	US-09-134-000C-5259
26	6	11.8	237	2	US-09-248-796A-14858
27	6	11.8	270	2	US-09-543-681A-4388

28	6	11.8	291	2	US-09-198-452A-373	Sequence 373, App
29	6	11.8	291	2	US-09-438-185A-359	Sequence 359, App
30	6	11.8	297	2	US-09-902-540-15551	Sequence 15551, A
31	6	11.8	304	2	US-09-328-352-7098	Sequence 7098, Ap
32	6	11.8	311	1	US-08-602-359A-41	Sequence 41, Appl
33	6	11.8	346	2	US-09-270-767-46598	Sequence 46598, A
34	6	11.8	379	2	US-10-104-047-3298	Sequence 3298, Ap
35	6	11.8	391	2	US-09-270-767-58641	Sequence 58641, A
36	6	11.8	398	2	US-09-538-092-501	Sequence 501, App
37	6	11.8	398	2	US-09-487-558B-404	Sequence 404, App
38	6	11.8	456	2	US-09-634-238-276	Sequence 276, App
39	6	11.8	476	2	US-09-248-796A-15175	Sequence 15175, A
40	6	11.8	483	2	US-09-902-540-9827	Sequence 9827, Ap
41	6	11.8	499	2	US-08-985-492-14	Sequence 14, Appl
42	6	11.8	499	2	US-09-949-016-5906	Sequence 5906, Ap
43	6	11.8	502	2	US-09-949-016-10424	Sequence 10424, A
44	6	11.8	572	2	US-10-104-047-3907	Sequence 3907, Ap
45	6	11.8	608	2	US-09-270-767-43297	Sequence 43297, A

ALIGNMENTS

RESULT 1

US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: SHU, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match 100.0%; Score 51; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWGCQSQNEVFDLLHACIPQLRCSNTTPTLTQRYCNASVTNSVKG 51
Db 1 MLQWGCQSQNEVFDLLHACIPQLRCSNTTPTLTQRYCNASVTNSVKG 51

RESULT 2

US-09-949-016-11115
; Sequence 11115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11115
; LENGTH: 192
; TYPE: PRN
; ORGANISM: Human
US-09-949-016-11115

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Query Match      100.0%; Score 51; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MLQMGQCSQNEYFDSLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKG 51

Db 9 MLOWAGCSQNEYFDSLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKG 59

RESULT 3
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

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Query Match          94.1%; Score 48; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.9e-44;
Matches 48: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	4	MAGQCSQNEYFDSLHACIPQIRCSSNTPTLTQRYCNASVTNSVKG	51
Dh	1	MAGQCSQNEYFDSLHACIPQIRCSSNTPTLTQRYCNASVTNSVKG	48

RESULT 4
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent NO. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACTI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 94.1%; Score 48; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.3e-43;
Matches 48; Conservative 0; Mismatches 0; Indels

QY 4 MAGCQSQNEYFDSLHACIPCOIRCSSNTPLTQRYCNASVTNSVKG 51
|||||
1 MAGCQSQNEYFDSLHACIPCOIRCSSNTPLTQRYCNASVTNSVKG 48
|||

RESULT 5
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 94.1%; Score 48; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.4e-43;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51
| | | | |
DH 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 48
| | | | |

RESULT 6
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match	86.3%;	Score 44;	DB 2;	Length 58;
Best Local Similarity	100.0%;	Pred. No. 1.6e-39;		
Matches 44:	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 8 CSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASVTNSVKG 51
|||
pB 1 CSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASVTNSVKG 44
|||

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RESULT 7
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-7

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Query Match 66.7%; Score 34; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.1e-29;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
DB 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

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RESULT 8
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
; US-09-854-864-13

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Query Match 66.7%; Score 34; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.6e-29;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
DB 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

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RESULT 9
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:

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; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
; US-09-854-864-12

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Query Match 19.6%; Score 10; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 12 EYFDSLHAC 21
DB 5 EYFDSLHAC 14

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RESULT 10

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US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-565-423-17

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Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 12 EYFDSLHAC 21
DB 9 EYFDSLHAC 18

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RESULT 11

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US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039

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; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 19.6%; Score 10; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSLHAC 21
Db 9 EYFDSLHAC 18
|||||

RESULT 12

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 19.6%; Score 10; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EYFDSLHAC 21
Db 9 EYFDSLHAC 18
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RESULT 13

US-09-270-767-60339
; Sequence 60339, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60339
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60339

Query Match 11.8%; Score 6; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRCSSN 31
Db 2 LRCSSN 7
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RESULT 14

US-09-621-976-5704
; Sequence 5704, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5704
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -43...-1
US-09-621-976-5704

Query Match 11.8%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CSSNTP 33
Db 49 CSSNTP 54
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RESULT 15

US-09-510-252-2
; Sequence 2, Application US/09510252
; Patent No. 6372490
; GENERAL INFORMATION:
; APPLICANT: Mandabalan, Krishnan
; APPLICANT: Yang, Meijia
; APPLICANT: Schulz, Vincent
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
; FILE REFERENCE: 15966-524 MDM US
; CURRENT APPLICATION NUMBER: US/09/510,252
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: USSN 60/121,192
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: USSN 60/122,643
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Any X can be any amino acid.
US-09-510-252-2

Query Match 11.8%; Score 6; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CQLRCS 29

Db 44 CQRCs 49

Search completed: March 2, 2006, 04:29:06
Job time : 47 secs

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Run on: March 2, 2006, 04:20:42 ; Search time 235 Seconds
(without alignments)
153.115 Million cell updates/sec

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Perfect score: 51
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Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 0
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	184	1	TNR17_HUMAN
2	51	100.0	184	2	Q6PE46_homo sapien
3	10	19.6	185	1	TNR17_MOUSE
4	8	15.7	148	2	Q5JK76_ORYSA
5	8	15.7	499	2	Q88714_mus musculus
6	8	15.7	1674	2	Q80218_mus musculus
7	8	15.7	2850	2	Q80T03_MOUSE
8	7	13.7	140	2	Q800M3_MORAM
9	7	13.7	140	2	Q800M4_MORCH
10	7	13.7	140	2	Q800M5_MORCS
11	7	13.7	140	2	Q800M6_MORSA
12	7	13.7	175	2	Q8BH44_MOUSE
13	7	13.7	202	2	Q9JDQ3_HHIVI
14	7	13.7	206	2	Q8LX76_9DIPT
15	7	13.7	207	2	Q8AS74_HHIVI
16	7	13.7	258	2	Q8BH51_MOUSE
17	7	13.7	264	2	Q4YH48_PLABE
18	7	13.7	307	2	Q4YZ16_PLABE
19	7	13.7	307	2	Q5DIB6_EFICO
20	7	13.7	309	2	Q9WY79_THEMEA
21	7	13.7	333	2	Q678F3_9VIRU
22	7	13.7	385	2	Q6MT77_MYCMS
23	7	13.7	409	2	Q672Q5_HHIVI
24	7	13.7	411	2	Q5FW06_XENTR
25	7	13.7	412	2	Q5U4G6_MOUSE
26	7	13.7	412	2	Q8K3A5_MOUSE
27	7	13.7	412	2	Q8BH02_MOUSE
28	7	13.7	413	2	Q4HZP5_GIBZE
29	7	13.7	457	2	Q8AVS9_XENLA
30	7	13.7	804	2	Q8WRL8_TETTH
31	7	13.7	945	2	Q52F58_MAGGR

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RESULT 1
TNR17_HUMAN
ID TNR17_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).
DE Name=TNFRSF17; Synonyms=BCM, BCMA;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RS NUCLEOTIDE SEQUENCE, AND CHROMOSOMAL TRANSLOCATION.
RC TISSUE=Lymph node, and Peripheral blood leukocyte.
RX MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbone F., Brouet J.C., Berger R., Larsen C.-J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
RL EMBO J. 11:3897-3904(1992).
RN [2]
RS NUCLEOTIDE SEQUENCE.
RC MEDLINE=94218235; PubMed=8165126;
RX Laabi Y., Gras M.P., Brouet J.C., Larsen C.-J., Tsapis A.;
RT "The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";
RL Nucleic Acids Res. 22:1147-1154(1994).
RN [3]
RS NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;
RX Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler B.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
RN [4]
RS NUCLEOTIDE SEQUENCE, AND VARIANT THR-153.
RC MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;
RX Kawasaki A., Teuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";
RL Genes Immun. 2:276-279(2001).
RN [5]
RS NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65; VAL-75; ASN-81 AND SER-165.
RX Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,

Q9PWC6 gallus gall
Q9R085 ratu musc
Q80TY6 mus muscu
Q5ZKD8 gallus gall
Q9Y4E8 homo sapien
Q8T5H1 mus muscu
Q80UK9 mus muscu
Q4RWH0 tetraodon n
Q8BB7_ORYSA
Q7XHD6_ORYSA
Q5AG18_DICTDI
Q8MTP3 encephalito
Q8UW83 paralichthy
Q93457 scophthalmu

RA Sherwood J.K., Sherwood A.M., Leitchauer B.J., Nickerson D.A.;
RT "NIH-SNPs, environmental genome project, NIH S515478, Department
of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ Databases.
RN [6]
RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
RX MEDLINE=20363816; PubMed=1903733;
RA Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
RA Inoue J.-I., Devergne O., Tsapis A.;
RT "TNF receptor family member BCMA (B cell maturation) associates with
TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
activates NF-kappa-B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
activated protein kinase.";
RN Immunol. 165:1322-1330(2000).
RP FUNCTION.
RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;
RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
Madden K., Xu W., Parikh-Novak J., Foster D., Lofton-Day C.,
Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
Harrison K., Kindsvogel W., Clegg C.H.;
RT "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
autoimmune disease.";
RN Nature 404:995-999(2000).
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theil L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
humoral immunity.";
RN Nat. Immunol. 1:252-256(2000).
RP INTERACTIONS WITH TRAF5 AND TRAF6.
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
RA Shu H.-B., Johnson H.;
RT "B cell maturation protein is a receptor for the tumor necrosis factor
family member TALL-1";
RN Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
CC -!- FUNCTION: Receptor for TNFSF13B/BLYS/BAPF and TNFSF13/APRIL.
CC Promotes B-cell survival and plays a role in the regulation of
humoral immunity. Activates NF-kappa-B and JNK.
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- INTERACTION:
CC O9Y275;TNFSF13B; NExp-1; Intact=EBI-519945, EBI-519169;
CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
and perinuclear Golgi-like structures.
CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
cells or monocytes.
CC -!- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a
form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation
t(4;16)(q26;pl3) with IL2.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; Z14954; CAA78679.1; -; mRNA.
CC EMBL; Z29575; CAAB2691.1; -; mRNA.
CC EMBL; Z29574; CAAB2690.1; -; Genomic DNA.
CC EMBL; U95742; AAB67251.1; -; Genomic DNA.
CC EMBL; AB052772; BAB60895.1; -; Genomic DNA.
CC EMBL; AY509112; AAR84240.1; -; Genomic DNA.
CC FIB; S43486; S43486.
CC PDB; 1QOD; X-ray; K/L/M/N/O/P/Q/R=8-46.
CC PDB; 1XU2; X-ray; R/S/T=5-51.
CC IntAct; Q02223; -;
CC Ensembl; ENSG00000048462; Homo sapiens.
CC HGNC; HGNC:11913; TNFRSF17.

DR MIM; 109545; -; C:integral to membrane; TAS.
DR GO; GO:0016021; C:plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004872; P:receptor activity; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0007145; P:signal transduction; TAS.
DR InterPro; IPR001368; TNFR_C6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE NEG.
KW 3D-structure; Chromosomal translocation; Immune response;
KW Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
FT TOPO_DOM 1 54 Extracellular (Potential)
FT TRANSMEM 55 77 Signal-anchor for type III membrane
FT protein (Potential).
FT TOPO_DOM 78 184 Cytoplasmic (Potential).
FT REPEAT 7 41 TNFR-Cys.
FT SITE 3 4 Breakpoint for translocation to form
FT DISULFID 8 21 IL2/TNFRSF17 oncogene.
FT DISULFID 24 37 By similarity.
FT DISULFID 28 41 By similarity.
FT VARIANT 54 54 A -> V.
FT VARIANT 65 65 /FTid=VAR_018755.
FT VARIANT 75 75 I -> V.
FT VARIANT 81 81 /FTid=VAR_018756.
FT VARIANT 153 153 S -> N (in dbSNP:373496).
FT VARIANT 165 165 A -> T.
FT VARIANT 165 165 /FTid=VAR_012234.
FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;
Query Match 100.0%; Score 51; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.4e-47;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQVAGQCSQNEYFDLSLLHACIPQLCRSSNTPPLTCORYCNASVTNSVKG 51
DB 1 MLQVAGQCSQNEYFDLSLLHACIPQLCRSSNTPPLTCORYCNASVTNSVKG 51
RESULT 2
QSP46 HUMAN
ID Q6PE46_HUMAN PRELIMINARY; PRT; 184 AA.
AC Q6PE46;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 17.
GN Name=TNFRSF17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Poolled;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketting A.C., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Poolled;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC058291; AAHS291.1; -; mRNA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;
 Query Match 100.0%; Score 51; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.4e-47; Indels 0;
 Matches 51; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 MLQAGQCSQNEYFSLHACIPQLRCSSNTPLTCQRYCNASVTSYK 51
 DB 1 MLQAGQCSQNEYFSLHACIPQLRCSSNTPLTCQRYCNASVTSYK 51
 RESULT 3
 TNR17 MOUSE
 ID TNR17 MOUSE STANDARD; PRT; 185 AA.
 AC 088472;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN Name=TNfrsf17; Synonyms=Bcm, Bcma;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698; DOI=10.1093/intimm/10.11.1693;
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
 RA Le Coniat M., Mornon J.P., Berger R., Tsapis A.,
 RT "The characterization of murine BCMA gene defines it as a new member
 RL of the tumor necrosis factor receptor superfamily."
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=22354683; PubMed=1246651; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziera R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Havaehizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettingman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for TNFSF13B/Blys/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O88472-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O88472-2; Sequence=VSP_006507;
 CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF061505; AAC23799.1; -; mRNA.
 CC EMBL; AK020247; BAB32038.1; -; mRNA.
 CC EMBL; BC027519; AAH27519.1; -; mRNA.
 CC HSSP; 002223; LOOP.
 CC Ensembl; ENSMUSG00000022496; Mus musculus.
 CC MGI; MGI:1343050; Tnfrsf17.
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC InterPro; IPR001368; TNFR_C6.
 CC PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
 CC PROSITE; PS00650; TNFR_NGFR_2; FALSE NEG.
 CC Alternative splicing; Immune response; Receptor; Signal-anchor;
 CC Transmembrane.
 CC TOPO DOM 1 49 Extracellular (Potential).
 CC TRANSMEM 50 70 Signal-anchor for type III membrane

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FT TORO DOM 71 185 protein (Potential).
FT REPEAT 4 36 Cytoplasmic (Potential).
FT DISULFID 5 18 TNFR-Cys.
FT DISULFID 21 32 By similarity.
FT DISULFID 25 36 By similarity.
FT VARSPLIC 87 91 Missing (in isoform 2).
FT /FTId=VSP_006507.
SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 19.6%; Score 10; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EYFDSLHAC 21
Db 9 EYFDSLHAC 18

RESULT 4
Q5JK76 ORYSA PRELIMINARY; PRT; 148 AA.
AC Q5JK76;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein OSUNBA0024F24.16 (Hypothetical protein B1156H12.31).
GN Name=OSJNBa0024F24.16; Synonym=B1156H12.31;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saij S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP004258; BAD88121.1; -; Genomic DNA.
DR EMBL; AP004225; BAD88061.1; -; Genomic DNA.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16215 MW; DB06C14D76E647CE CRC64;

Query Match 15.7%; Score 8; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 SILHACIP 23
Db 135 SILHACIP 142

RESULT 5
O88714 MOUSE PRELIMINARY; PRT; 499 AA.
ID O88714 MOUSE PRELIMINARY;
AC O88714;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gastric mucin-like protein (Fragment).
GN Name=Muc6; Synonym=gastri mucin-like;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Stomach;
RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
RA Rio M.C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Stomach;
RA Tomasetto C.L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010752; CAA09343.1; -; mRNA.
DR HSSP; P56682; ICCV.
DR Ensembl; ENSMUSG00000048191; Mus musculus.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR002919; Prot_Inh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00216; VWD; 1.
DR NON_TER 1 499
FT NON_TER 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;
SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 15.7%; Score 8; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFD 15
Db 430 CSQNEYFD 437

RESULT 6
Q80Z18 MOUSE PRELIMINARY; PRT; 1674 AA.
ID Q80Z18 MOUSE PRELIMINARY;
AC Q80Z18;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted gel-forming mucin (Fragment).
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
RA Escande F., Buisine M.P.;
RT "The mouse secreted gel-forming mucin gene cluster.";
RL Biochim. Biophys. Acta 1676:240-250(2004).
DR EMBL; AJ511867; CAD54415.1; -; Genomic DNA.
DR EMBL; AJ511868; CAD54415.1; JOINED; Genomic DNA.
DR HSSP; O46162; 1KJ0.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR002919; Prot_Inh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
DR NON_TER 1674 1674

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SQ SEQUENCE 1674 AA; 181168 MW; 38C42CB004476309 CRC64;
Query Match 15.7%; Score 8; DB 2; Length 1674;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSONEYFD 15
DB 1181 CSONEYFD 1188

RESULT 7
Q80T03 MOUSE
ID Q80T03_MOUSE PRELIMINARY; PRT; 2850 AA.
AC Q80T03;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MUC6.
GN Name=Muc6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;
RA Desseyn J.-L., Laine A.;
RT "Characterization of mouse muc6 and evidence of conservation of the
RT gel-forming mucin gene cluster between human and mouse.";
RL Genomics 81:433-436(2003).
DR EMBL; AY184388; AAC47735.1; -; Genomic DNA.
DR EMBL; AY184385; AAC47735.1; JOINED; Genomic DNA.
DR EMBL; AY184387; AAC47735.1; JOINED; Genomic DNA.
DR EMBL; AY184386; AAC47735.1; JOINED; Genomic DNA.
DR HSSP; O46162; 1KJ0
DR Ensembl; ENSMUSG0000048191; Mus musculus.
DR MGI; MGI:2663233; Muc6.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR002919; ProtInh_CR_TIL.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS01225; CTCK 2; 1.
SQ SEQUENCE 2850 AA; 300398 MW; 9CD95F0845C79C9D CRC64;

Query Match 15.7%; Score 8; DB 2; Length 2850;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSONEYFD 15
DB 1222 CSONEYFD 1229

RESULT 8
Q800M3 MORAM
ID Q800M3_MORAM PRELIMINARY; PRT; 140 AA.
AC Q800M3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insulin-like growth factor I receptor (Fragment).
OS Morone americana (White perch).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OC NCBI_TaxID=46260;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Fruchtmann S., Hawkins M.B., Borski R.J.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC EMBL; AF402675; AAO73860.1; -; mRNA.
CC HSSP; P08069; 1JQH.
CC SMR; Q800M4; 1-140.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
CC InterPro; IPR000719; Prot_kinase.
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Fruchtmann S., Hawkins M.B., Borski R.J.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC EMBL; AF402675; AAO73860.1; -; mRNA.
CC HSSP; P08069; 1JQH.
CC SMR; Q800M4; 1-140.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
CC InterPro; IPR000719; Prot_kinase.
```

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DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008286; Tyr_kinase_AS.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
FT NON_TER 140
SQ SEQUENCE 140 AA; 15815 MW; AC3C1C98A1674D1B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQG 7
DB 103 MLQMAQG 109

RESULT 10
Q800M5 MORCS PRELIMINARY; PRT; 140 AA.
AC Q800M5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insulin-like growth factor I receptor (Fragment).
OS Morone chrysops x Morone saxatilis (White bass x Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=45352;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fruchtmann S., Hawkins M.B., Borski R.J.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC EMBL; AF402673; AAC73859.1; -; mRNA.
CC HSSP; P08069; IJOH.
CC SMR; Q800M5; 1-140.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
FT NON_TER 140
SQ SEQUENCE 140 AA; 15787 MW; BB1B2C98A17E541B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQG 7
DB 103 MLQMAQG 109

RESULT 11
Q800M6 MORSA PRELIMINARY; PRT; 140 AA.
AC Q800M6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insulin-like growth factor I receptor (Fragment).
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fruchtmann S., Hawkins M.B., Borski R.J.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC EMBL; AF402673; AAC73858.1; -; mRNA.
CC HSSP; P08069; IJOH.
CC SMR; Q800M6; 1-140.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
FT NON_TER 140
SQ SEQUENCE 140 AA; 15787 MW; BB1B2C98A17E541B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMAQG 7
DB 103 MLQMAQG 109

RESULT 12
Q8BHX4 MOUSE PRELIMINARY; PRT; 175 AA.
AC Q8BHX4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:4831418F03 product:HYPOTHETICAL 28.4 Kda PROTEIN
DE homolog (Fragment).
DE Name=Wdr32; Synonyms=AA959934;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=92729253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.; cDNA cloning.";
RT Meth. Enzymol. 303:19-44 (1999).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Head;
RA MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayata Y., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Head;
RA MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohtsuka N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076417; BAC36330.1; -; mRNA.
DR Ensembl; ENSMUSG0000035572; Mus musculus.
DR MGI; MGI:2140179; AA959334.
DR MGI; MGI:2140179; WDR32.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 1.
DR SMART; SM00320; WD40; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 175 AA; 19571 MW; D5A62B8785D9F10F CRC64;
Query Match 13.7%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 LRCSSNT 32
DB 43 LRCSSNT 49
RESULT 13
Q9JDO3 9HIV1 PRELIMINARY; PRT; 202 AA.
AC Q9JDO3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OC NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20027278; PubMed=10559367;
RA Shankarappa R., Margolick J.B., Gange S.J., Rodrigo A.G., Upchurch D.,
RA Parzadeegan H., Gupta P., Rinaldo C.R., Learn G.H., He X., Huang X.-L.,
RA Mullins J.I.;
RT "Consistent viral evolutionary changes associated with the progression
RT of human immunodeficiency virus type 1 infection.";
RL J. Virol. 73:10489-10502 (1999).
DR EMBL; AF137741; AAF31608.1; -; Genomic_RNA.
DR SNR; Q9JDO3; 1-202
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 202 AA; 22563 MW; OD9BBFE32B16B254 CRC64;
Query Match 13.7%; Score 7; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 QLRCSN 31
DB 171 QLRCSN 177
RESULT 14
Q8LX76 9DIPT
ID Q8LX76 9DIPT PRELIMINARY; PRT; 206 AA.
AC Q8LX76;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN Name=COI;

OS Chaoborus americanus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Chaoboridae;
OC Chaoborus.
OX NCBI_TaxID=204565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Berendonk T.U.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ427618; CAD44504.1; -; Genomic_DNA.
DR GO; GO:0005739; C.mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 206 AA; 23927 MW; E6BC8651E8AE571 CRC64;

Query Match 13.7%; Score 7; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 SSNTPEL 35
DB 137 SSNTPEL 143

RESULT 15
Q8AS74 9HIV1
ID Q8AS74_9HIV1 PRELIMINARY; PRT; 207 AA.
AC Q8AS74;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
OS Name=env;
GN Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Frey S., Gupta P., Learn G.H., Mittler J., Shriner D.,
RA Nickle D.C., Jensen M.A., Rodrigo A.G., Beerli P., He X., Zhao H.,
RA Rossini A., Felsenstein J., Walker B.D., Mullins J.I.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF535413; AAN07372.1; -; Genomic_RNA.
DR SMR; Q8AS74; 1-207.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 22946 MW; DCD2182D0A73F90B CRC64;

Query Match 13.7%; Score 7; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 QLRCSN 31
DB 174 QLRCSN 180

Search completed: March 2, 2006, 04:27:30
Job time : 237 secs